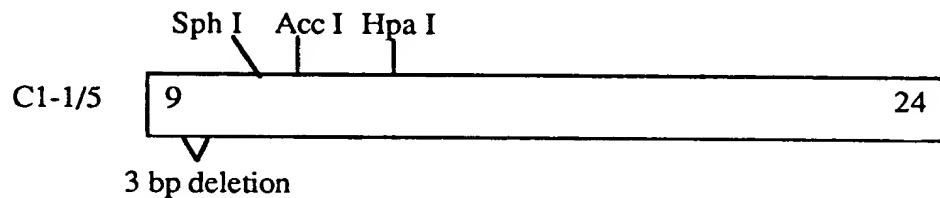
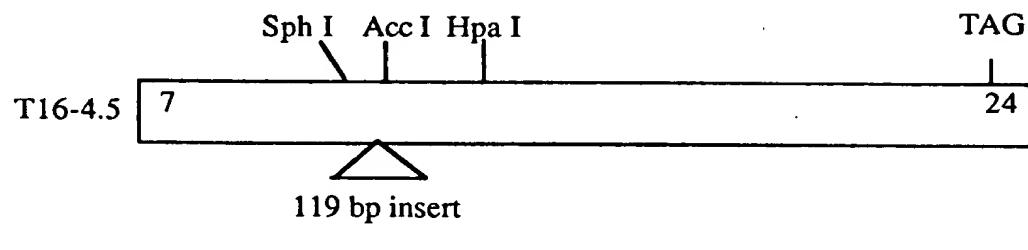
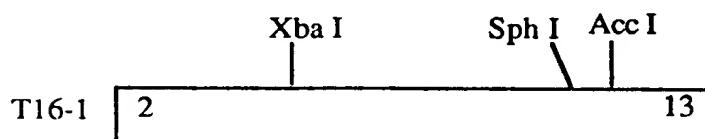
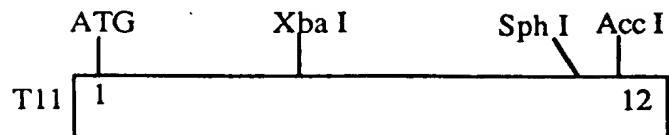


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**FIGURE 1**

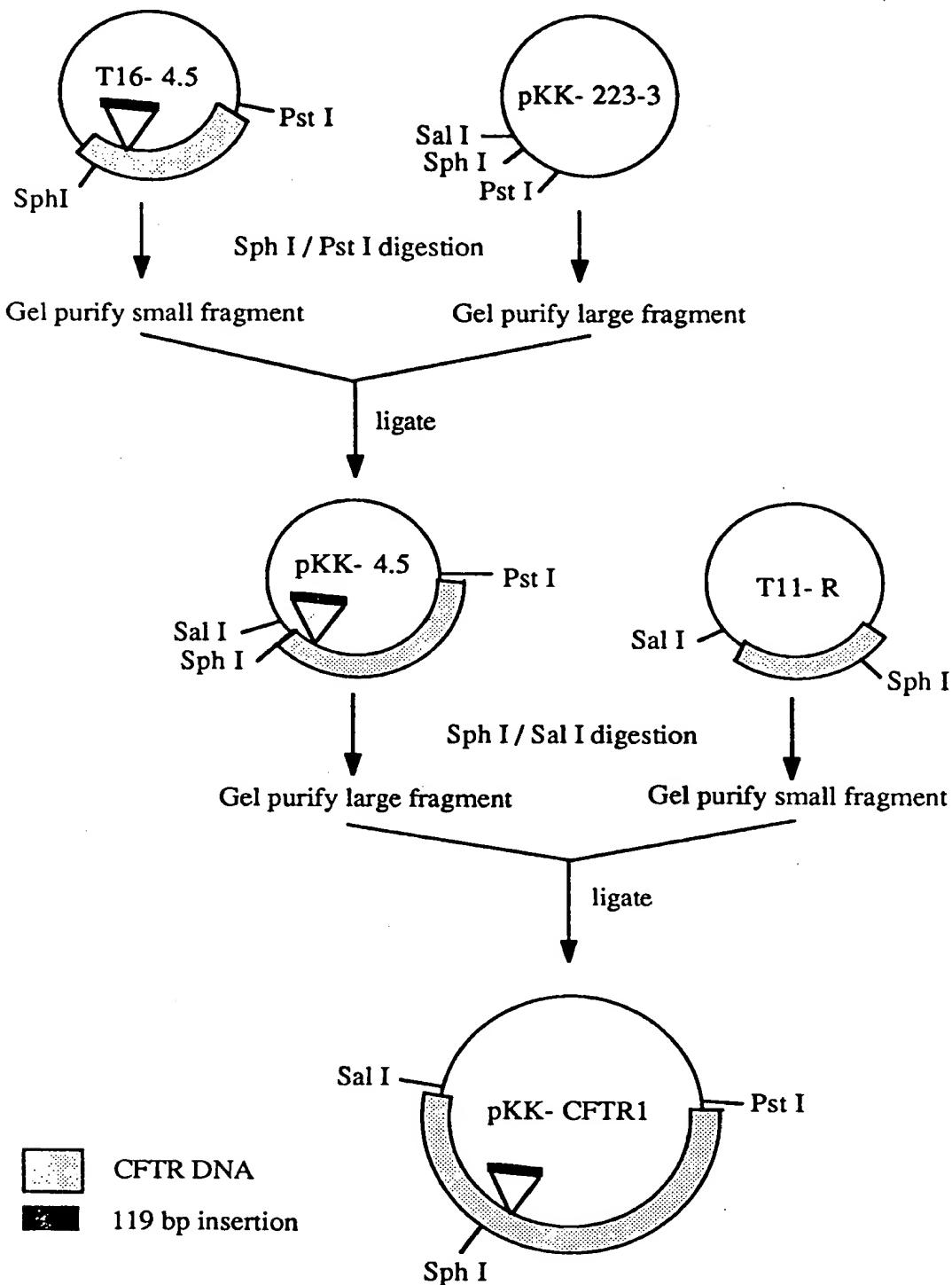
PARTIAL cDNA CLONES OF THE CFTR GENE



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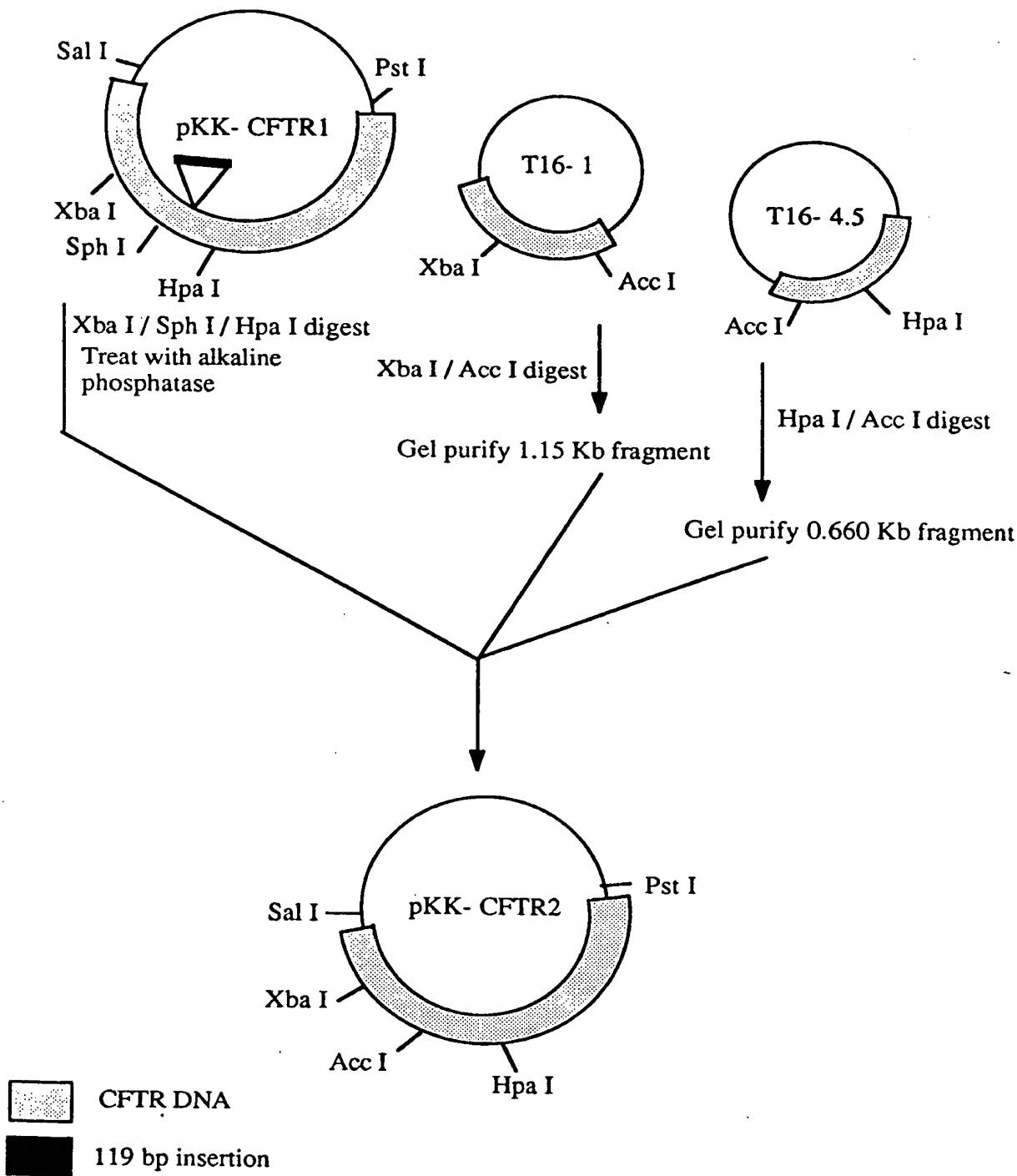
**FIGURE 2**  
STRATEGY FOR CONSTRUCTING pKK-CFTR1



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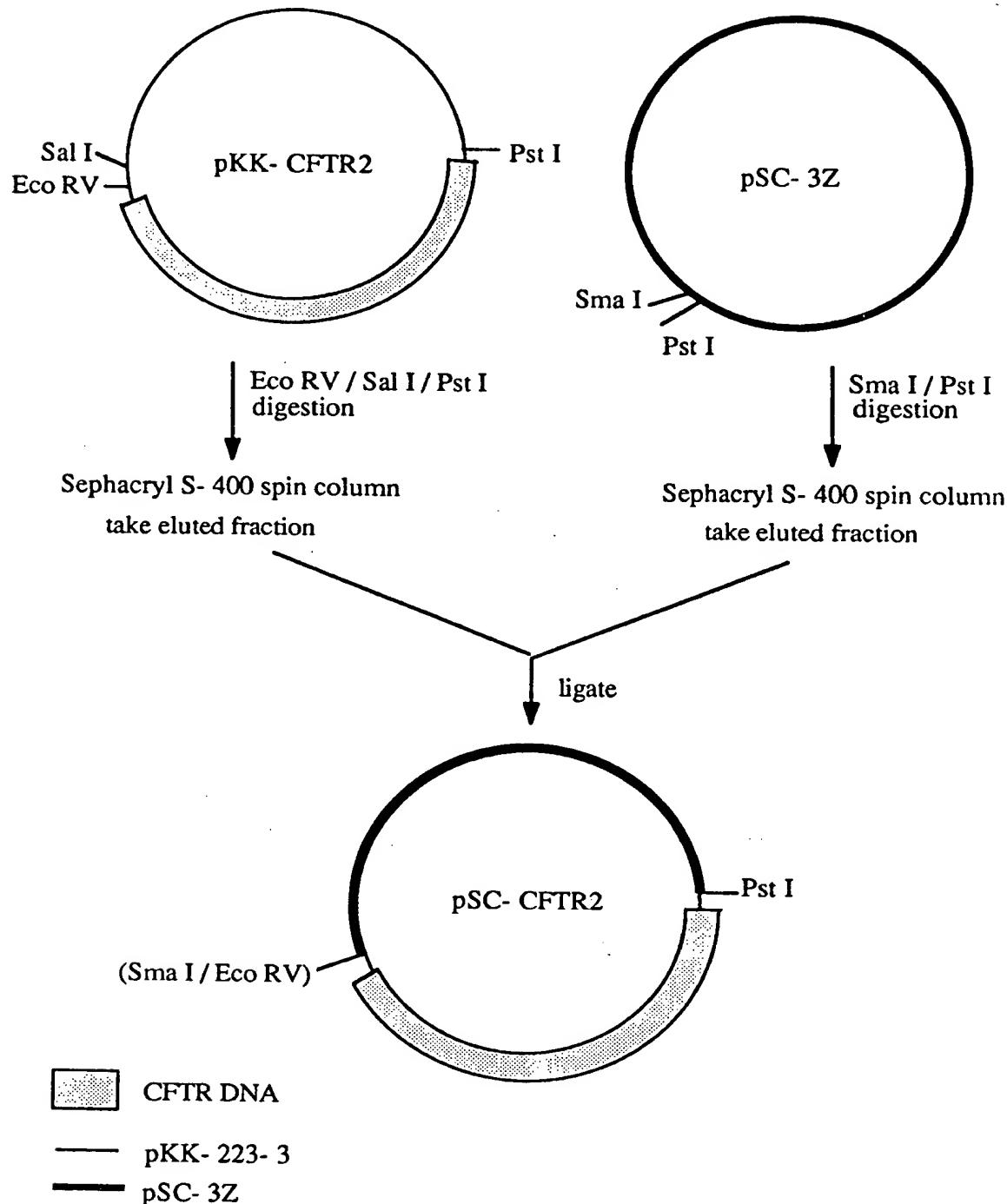
**FIGURE 3**  
**CONSTRUCTION OF THE pKK- CFTR2 PLASMID**



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**FIGURE 4**  
STRATEGY FOR CONSTRUCTING THE pSC- CFTR2 PLASMID

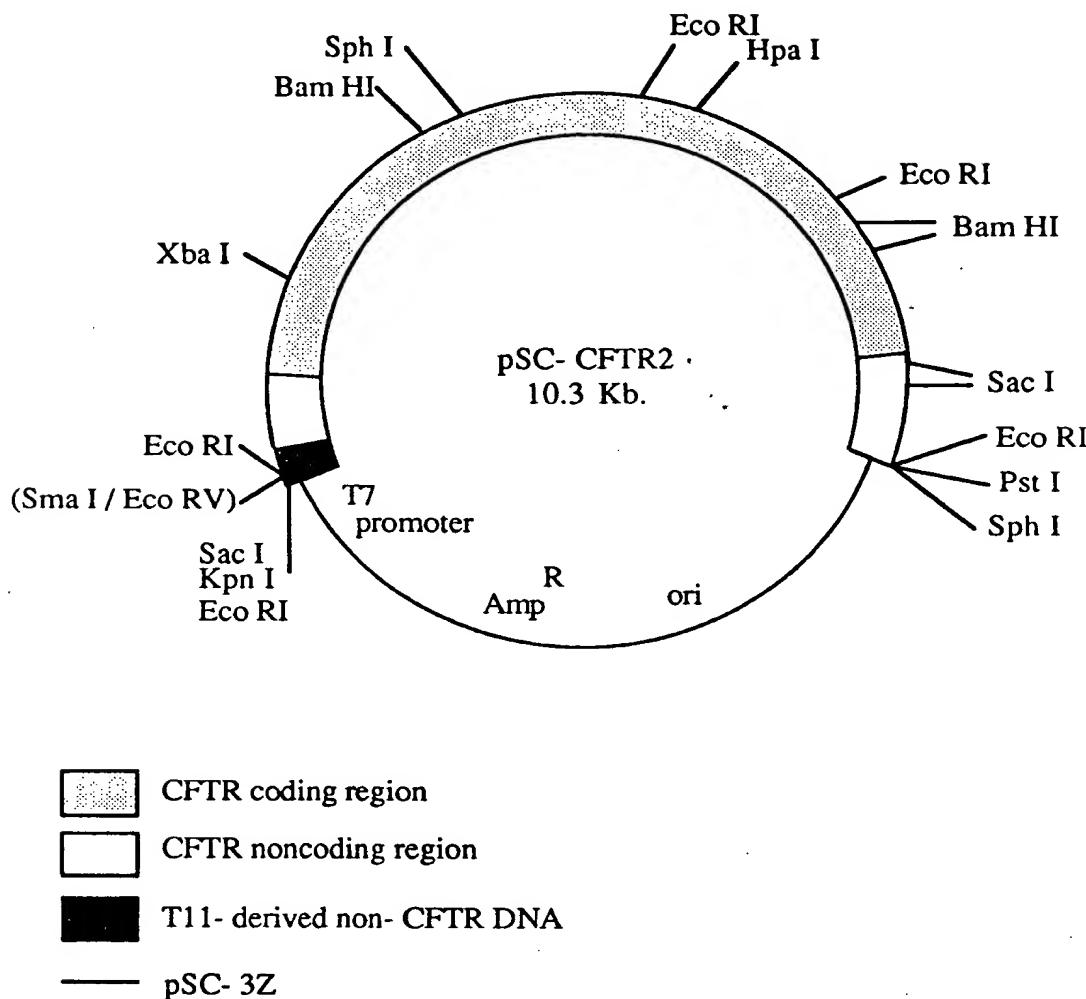


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**FIGURE 5**  
MAP OF pSC- CFTR2

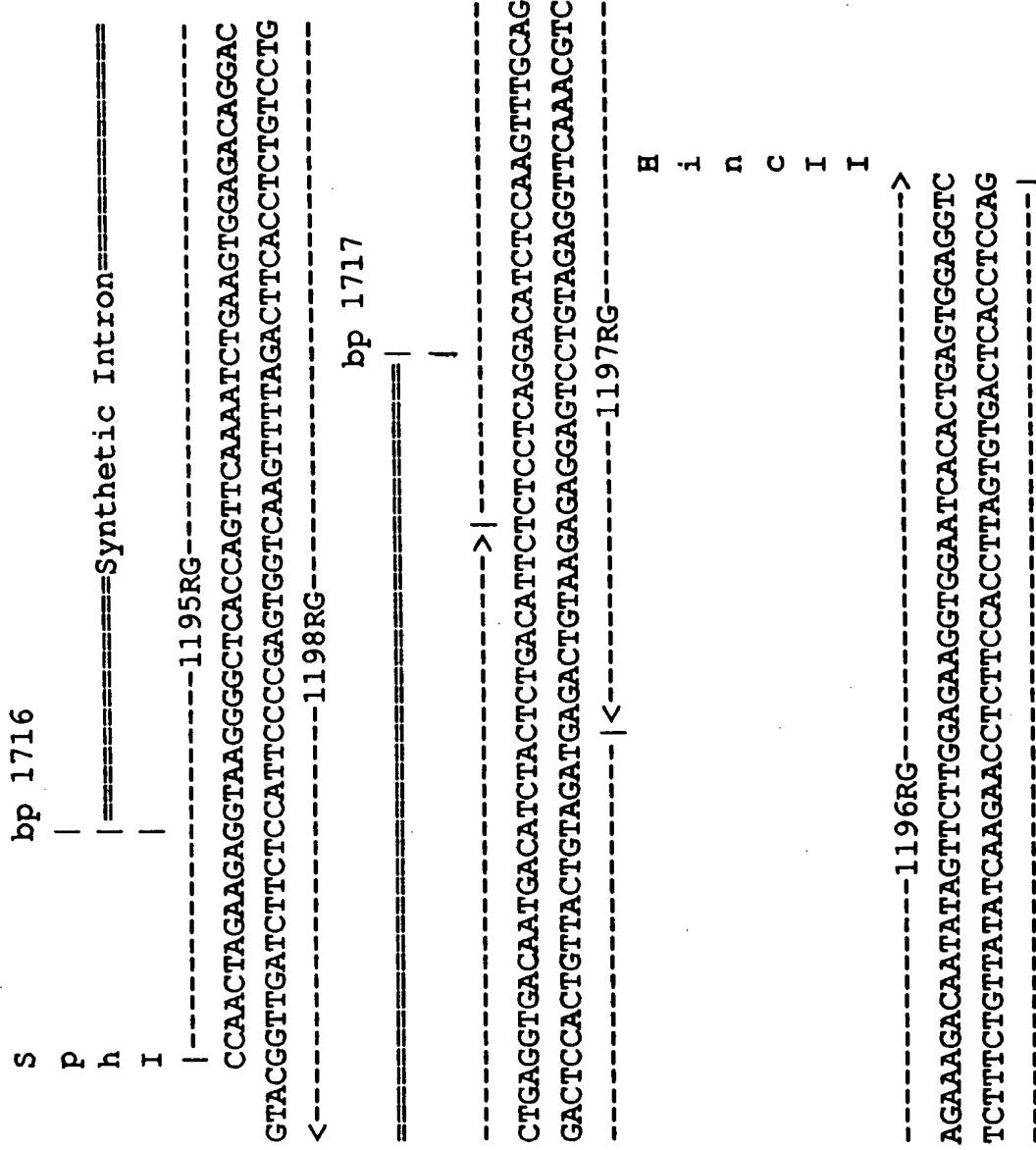


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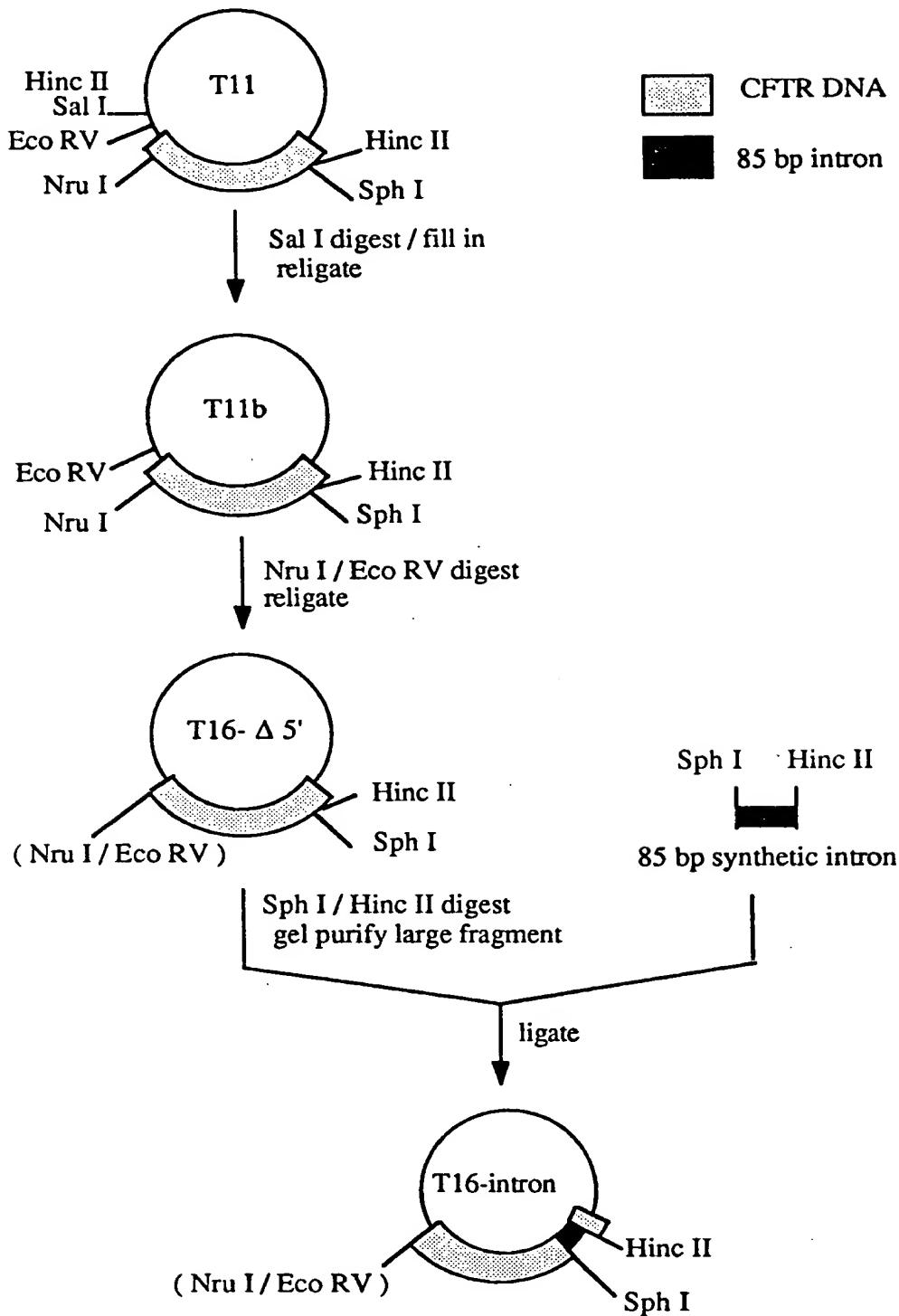
FIGURE 6



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CKV

**FIGURE 7A**  
CONSTRUCTION OF THE pKK-CFTR3 cDNA

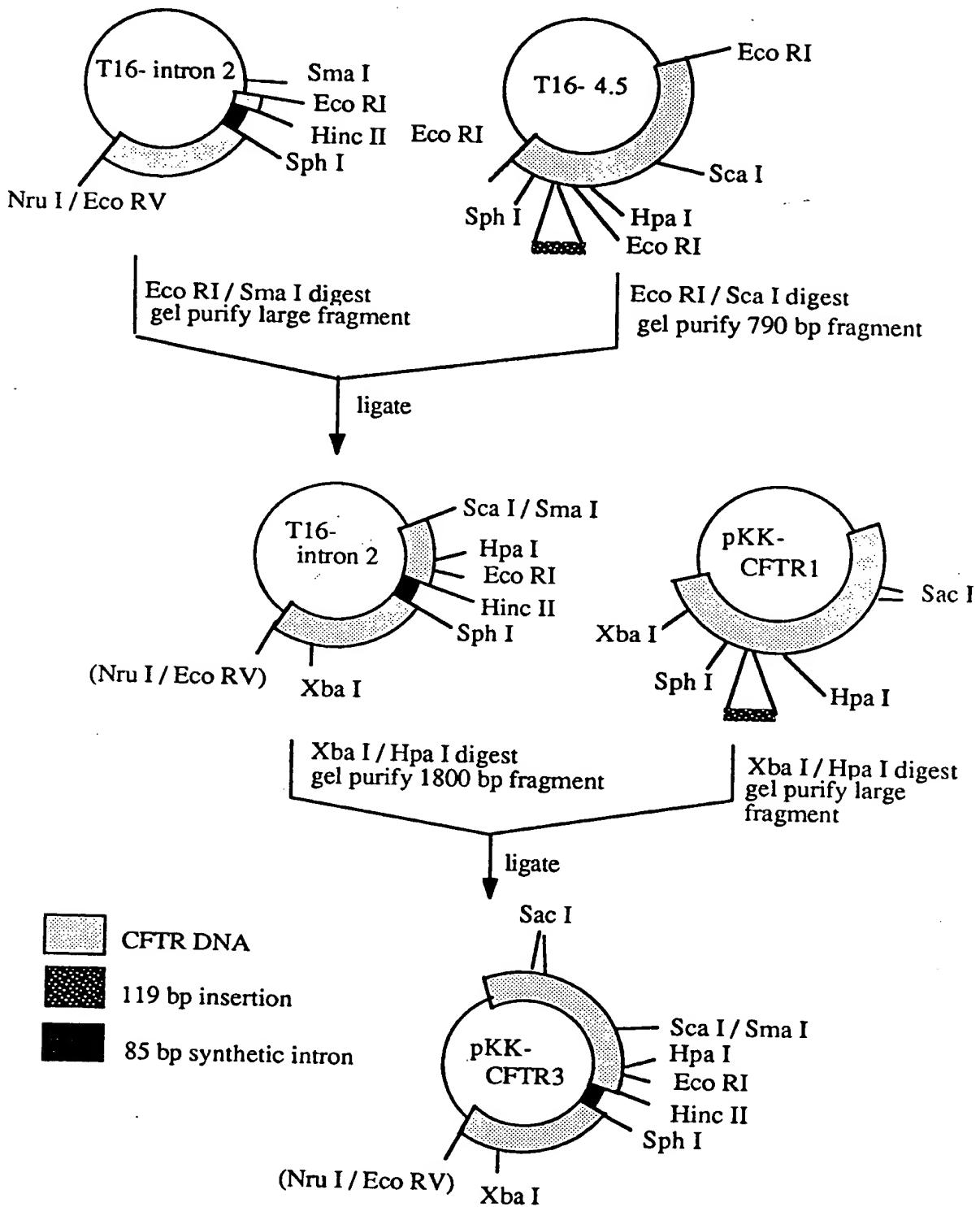


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**FIGURE 7B**

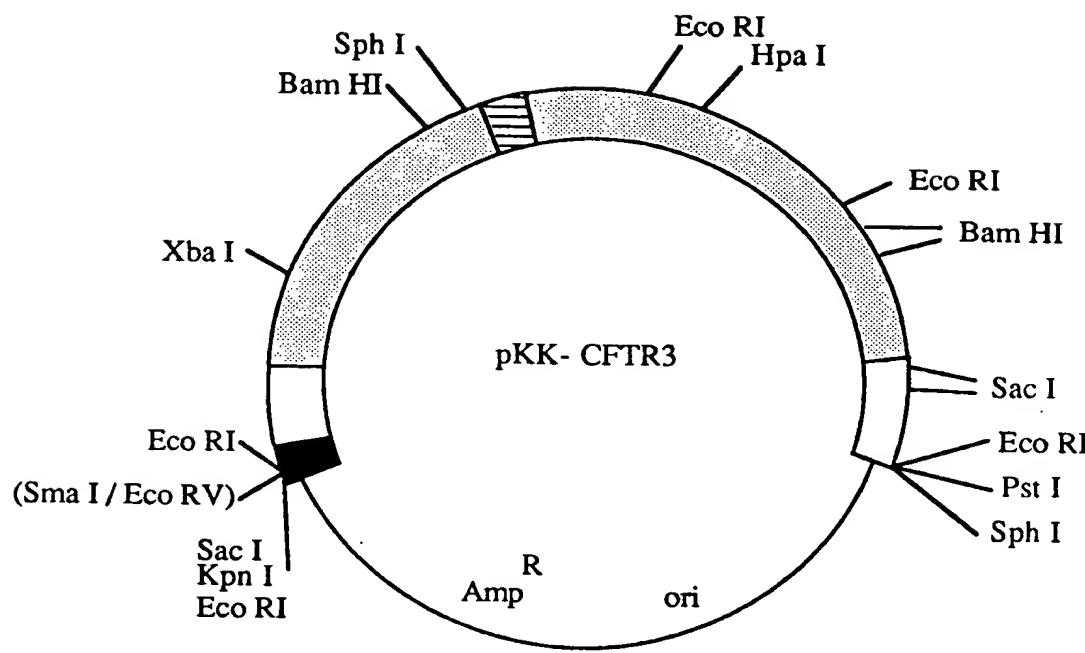
## CONSTRUCTION OF THE pKK-CFTR3 CLONE (cont'd.)



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**FIGURE 8**  
MAP OF pKK- CFTR3



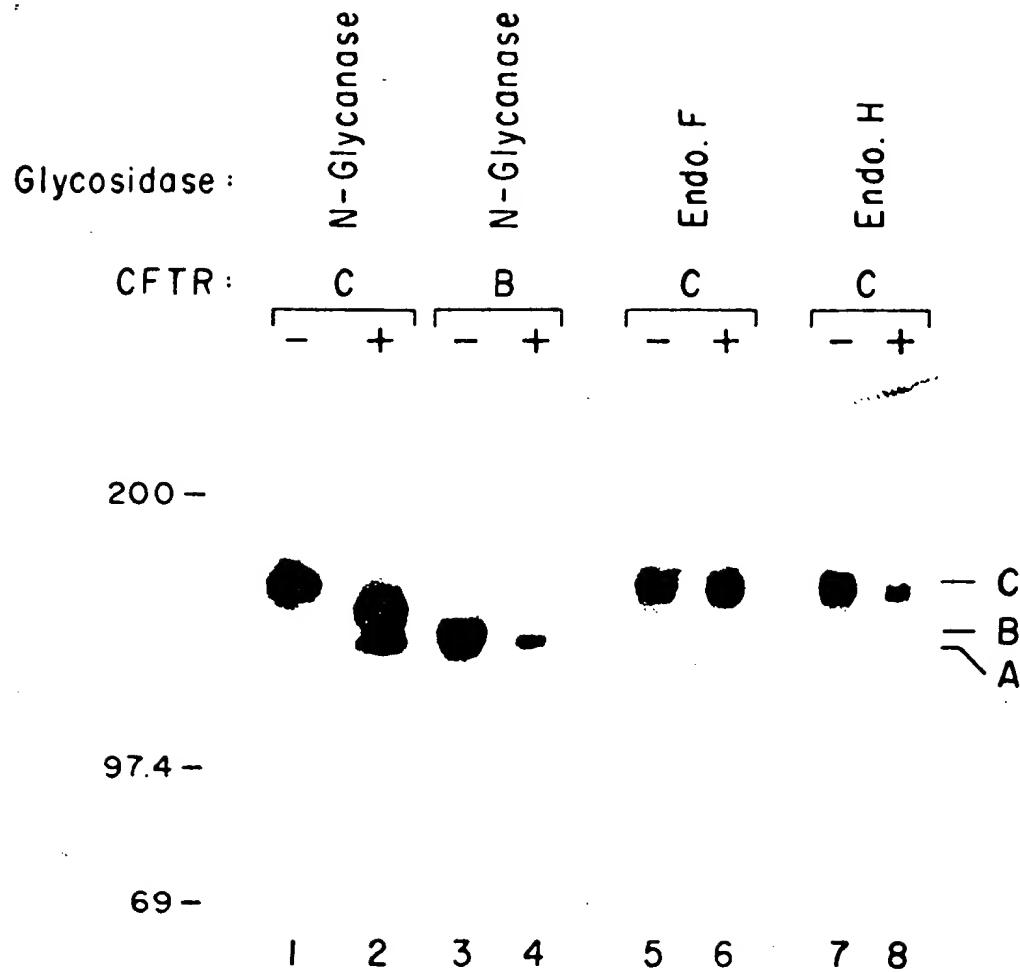
- [Solid white box] CFTR coding region
- [Hatched box] CFTR noncoding region
- [Horizontal stripes box] 85 bp intron
- [Solid black box] T11- derived non- CFTR DNA
- pKK- 223- 3

IG 4-9.2

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FIGURE 9

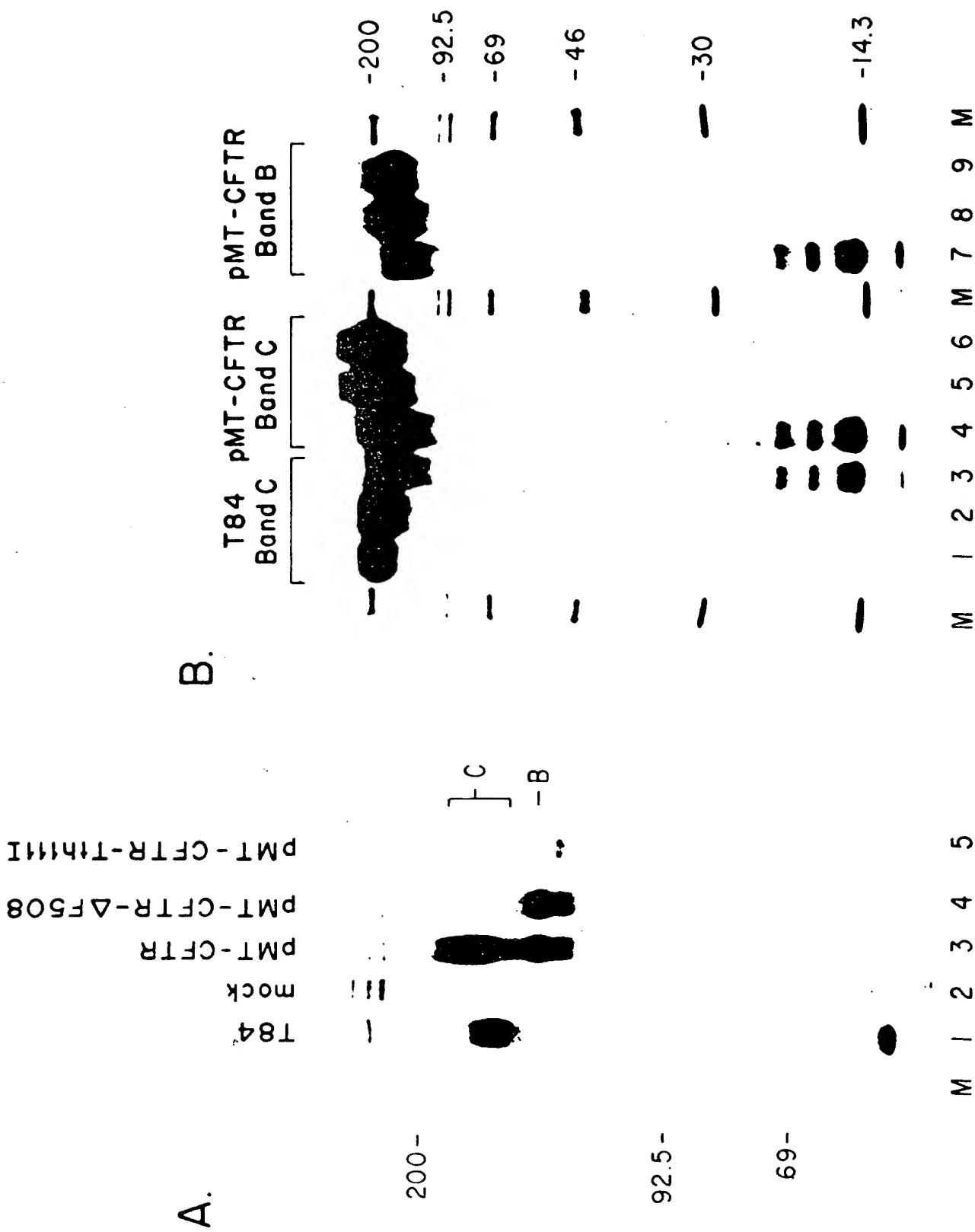


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over

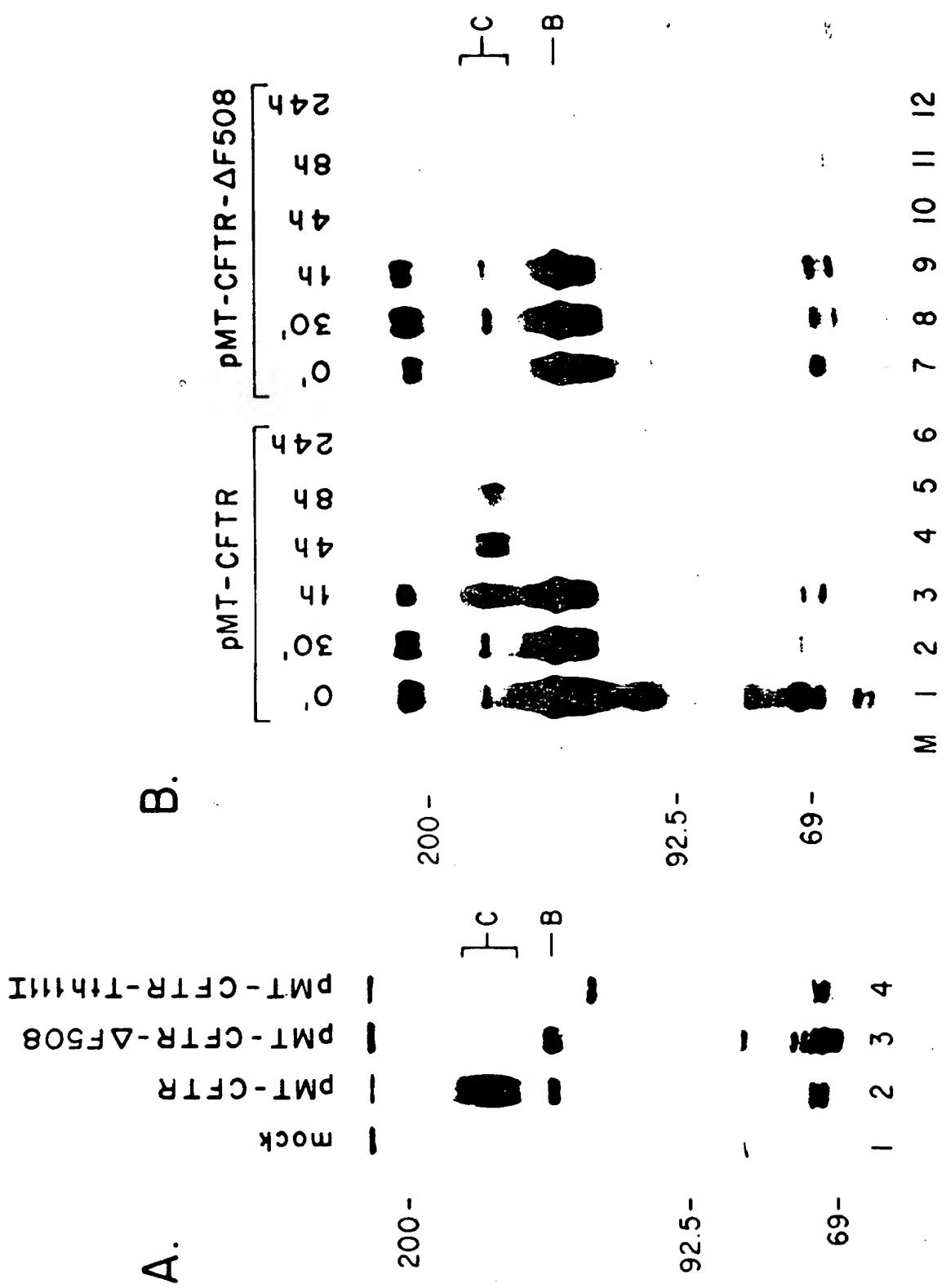
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FIGURE 10



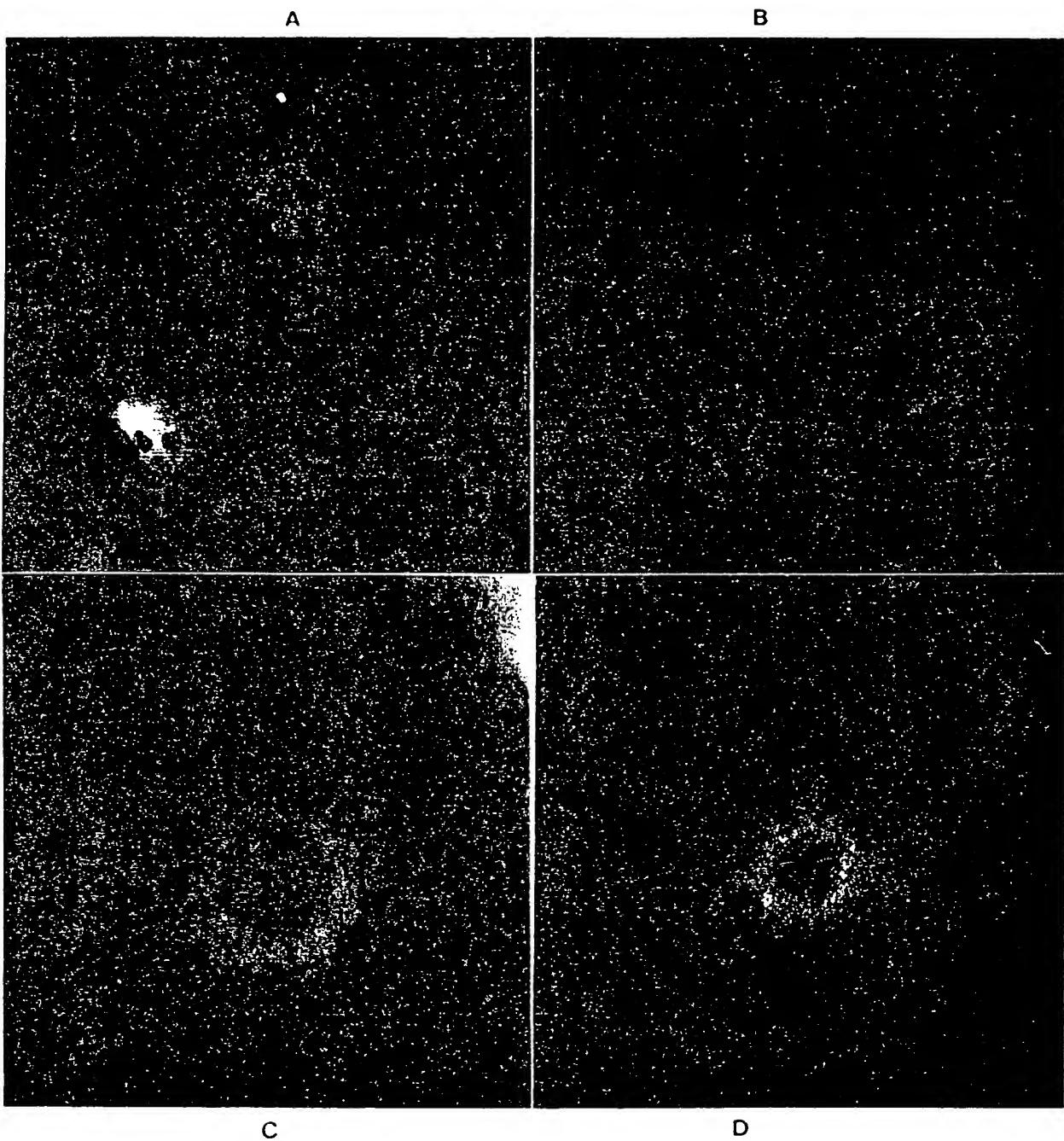
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## **FIGURE 11**



**FIGURE 12**

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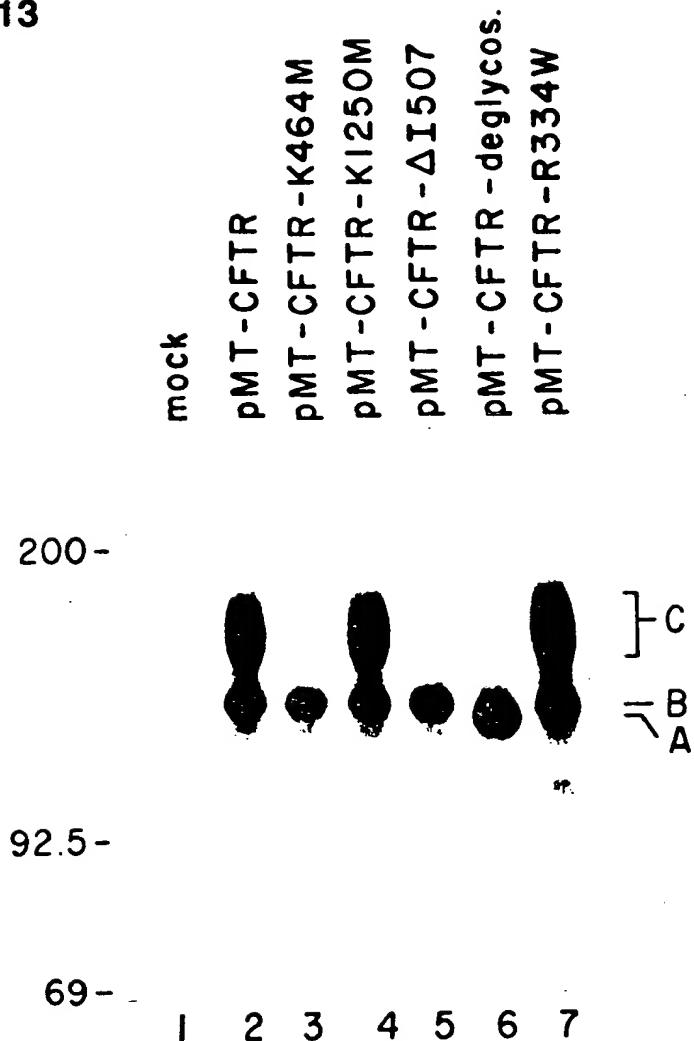


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FIGURE 13



IG 4-9.2

over

**TABLE 1** *Figure 15*

1	AATTGGAAGCAAATGACATCACAGCAGGTCAAGAGAAAAAGGG	42
43	TTGAGCGGCAGGCACCCAGAGTAGTAGGTCTTGCCATTAGG	84
85	AGCTTGAGCCCCAGACGGCCCTAGCAGGGACCCCAGCGCCCGA	126
1	MetGlnArgSerProLeuGluLysAlaSerValVal	12
127	GAGACCATGCAGAGGTCGCCTCTGGAAAAGGCCAGCGTTGTC	168
13	SerLysLeuPhePheSerTrpThrArgProIleLeuArgLys	26
169	TCCAAACTTTTTTCAGCTGGACCAGACCAATTGAGGAAA	210
27	GlyTyrArgGlnArgLeuGluLeuSerAspIleTyrGlnIle	40
211	GGATACAGACAGGCCCTGGAATTGTCAGACATATAACCAAATC	252
41	ProSerValAspSerAlaAspAsnLeuSerGluLysLeuGlu	54
253	CCTTCTGTTGATTCTGCTGACAATCTATCTGAAAAATTGGAA	294
55	ArgGluTrpAspArgGluLeuAlaSerLysLysAsnProLys	68
295	AGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAATCCTAAA	336
69	LeuIleAsnAlaLeuArgArgCysPhePheTrpArgPheMet	82
337	CTCATTAATGCCCTCGCGATGTTTCTGGAGATTATG	378
83	PheTyrGlyIlePheLeuTyrLeuGlyGluValThrLysAla	96
379	TTCTATGGAATCTTTATATTAGGGAAAGTCACCAAAGCA	420
97	ValGlnProLeuLeuLeuGlyArgIleIleAlaSerTyrAsp	110
421	GTACAGCCTCTCTACTGGGAAGAACATAGCTTCCTATGAC	462
111	ProAspAsnLysGluGluArgSerIleAlaIleTyrLeuGly	124
463	CCGGATAACAAGGAGGAACGCTCTATCGCGATTATCTAGGC	504
125	IleGlyLeuCysLeuLeuPheIleValArgThrLeuLeuLeu	138
505	ATAGGCTTATGCCCTCTCTTATTGTGAGGACACTGCTCCTA	546
139	HisProAlaIlePheGlyLeuHisHisIleGlyMetGlnMet	152
547	CACCCAGCCATTGGCCTTCATCACATTGGAATGCAGATG	588
153	ArgIleAlaMetPheSerLeuIleTyrLysLysThrLeuLys	166
589	AGAATAGCTATGTTAGTTGATTATAAGAAGACTTAAAG	630
167	LeuSerSerArgValLeuAspLysIleSerIleGlyGlnLeu	180
631	CTGTCAAGCCGTGTTCTAGATAAAATAAGTATTGGACAACTT	672
181	ValSerLeuLeuSerAsnAsnLeuAsnLysPheAspGluGly	194
673	GTTAGTCTCCTTCCAACAAACCTGAACAAATTGATGAAGGA	714

195	LeuAlaLeuAlaHisPheValTrpIleAlaProLeuGlnVal	208
715	CTTGCATTGGCACATTCGTGTGGATCGCTCCTTGCAAGTG	756
209	AlaLeuLeuMetGlyLeuIleTrpGluLeuLeuGlnAlaSer	222
757	GCACTCCTCATGGGGCTAACATCTGGGAGTTACAGGCGTCT	798
223	AlaPheCysGlyLeuGlyPheLeuIleValLeuAlaLeuPhe	236
799	GCCTTCTGTGGACTTGGTTCTGATAGTCCTGCCCTTTT	840
237	GlnAlaGlyLeuGlyArgMetMetLysTyrArgAspGln	250
841	CAGGCTGGGCTAGGGAGAAATGATGATGAAGTACAGAGATCAG	882
251	ArgAlaGlyLysIleSerGluArgLeuValIleThrSerGlu	264
883	AGAGCTGGGAAGATCAGTGAAAGACTTGTGATTACCTCAGAA	924
265	MetIleGluAsnIleGlnSerValLysAlaTyrCysTrpGlu	278
925	ATGATTGAAAATATCCAATCTGTTAAGGCATACTGCTGGAA	966
279	GluAlaMetGluLysMetIleGluAsnLeuArgGlnThrGlu	292
967	GAAGCAATGGAAAAAAATGATTGAAAACCTTAAGACAAACAGAA	1008
293	LeuLysLeuThrArgLysAlaAlaTyrValArgTyrPheAsn	306
1009	CTGAAACTGACTCGGAAGGCAGCCTATGTGAGATACTTCAAT	1050
307	SerSerAlaPhePhePheSerGlyPhePheValValPheLeu	320
1051	AGCTCAGCCTTCTTCTCAGGGTTCTTGTGGTGTNTTA	1092
321	SerValLeuProTyrAlaLeuIleLysGlyIleIleLeuArg	334
1093	TCTGTGCTTCCCTATGCACTAACAGGAATCATCCTCCGG	1134
335	LysIlePheThrThrIleSerPheCysIleValLeuArgMet	348
1135	AAAATATTCACCACCATCTCATTGCAATTGTTCTGCGCATG	1176
349	AlaValThrArgGlnPheProTrpAlaValGlnThrTrpTyr	362
1177	GCGGTCACTCGGCAATTCCCTGGGCTGTACAAACATGGTAT	1218
363	AspSerLeuGlyAlaIleAsnLysIleGlnAspPheLeuGln	376
1219	GACTCTTGGAGCAATAAACAAAATACAGGATTCTTACAA	1260
377	LysGlnGluTyrLysThrLeuGluTyrAsnLeuThrThrThr	390
1261	AAGCAAGAATATAAGACATTGGAATATAACTAACGACTACA	1302
391	GluValValMetGluAsnValThrAlaPheTrpGluGluGly	404
1303	GAAGTAGTGTGGAGAAATGTAACAGCCTCTGGGAGGAGGGA	1344
405	PheGlyGluLeuPheGluLysAlaLysGlnAsnAsnAsnAsn	418
1345	TTTGGGAATTATTGAGAAAGCAAAACAAAACAATAACAAT	1386

419	ArgLysThrSerAsnGlyAspAspSerLeuPhePheSerAsn	432
1387	AGAAAAAACTTCTAATGGTGATGACAGCCTCTTCAGTAAT	1428
433	PheSerLeuLeuGlyThrProValLeuLysAspIleAsnPhe	446
1429	TTCTCACTTCTGGTACTCCTGTCCTGAAAGATATTAATTTC	1470
447	LysIleGluArgGlyGlnLeuLeuAlaValAlaGlySerThr	460
1471	AAGATAAGAGGACAGTTGTTGGCGGTTGCTGGATCCACT	1512
461	GlyAlaGlyLysThrSerLeuLeuMetMetIleMetGlyGlu	474
1513	GGAGCAGGCAAGACTTCACTTCTAATGATGATTATGGGAGAA	1554
475	LeuGluProSerGluGlyLysIleLysHisSerGlyArgIle	488
1555	CTGGAGCCTTCAGAGGGTAAAATTAAGCACAGTGGAAAGAATT	1596
489	SerPheCysSerGlnPheSerTrpIleMetProGlyThrIle	502
1597	TCATTCTGTTCTCAGTTTCCTGGATTATGCCTGGCACCAT	1638
503	LysGluAsnIleIlePheGlyValSerTyrAspGluTyrArg	516
1639	AAAGAAAATATCATCTTGGTGTTCCTATGATGAATATAGA	1680
517	TyrArgSerValIleLysAlaCysGlnLeuGluGluAspIle	530
1681	TACAGAACGCGTCATCAAAGCATGCCAACTAGAACAGAGGACATC	1722
531	SerLysPheAlaGluLysAspAsnIleValLeuGlyGluGly	544
1723	TCCAAGTTGCAGAGAAAGACAATATAGTTCTGGAGAACGT	1764
545	GlyIleThrLeuSerGlyGlyGlnArgAlaArgIleSerLeu	558
1765	GGAATCACACTGAGTGGAGGTCAACGAGCAAGAATTCTTTA	1806
559	AlaArgAlaValTyrLysAspAlaAspLeuTyrLeuLeuAsp	572
1807	GCAAGAGCAGTATACAAAGATGCTGATTGTATTAGAC	1848
573	SerProPheGlyTyrLeuAspValLeuThrGluLysGluIle	586
1849	TCTCCTTGGATACCTAGATGTTAACAGAAAAAGAAATA	1890
587	PheGluSerCysValCysLysLeuMetAlaAsnLysThrArg	600
1891	TTTGAAAGCTGTGTCTGTAAACTGATGGCTAACAAAAACTAGG	1932
601	IleLeuValThrSerLysMetGluHisLeuLysLysAlaAsp	614
1933	ATTTGGTCACTTCTAAAATGGAACATTAAAGAAAGCTGAC	1974
615	LysIleLeuIleLeuHisGluGlySerSerTyrPheTyrGly	628
1975	AAAATATTAATTGGCATGAAGGTAGCAGCTATTGTTATGGG	2016
629	ThrPheSerGluLeuGlnAsnLeuGlnProAspPheSerSer	642
2017	ACATTTCAAGAACTCCAAAATCTACAGCCAGACTTAGCTCA	2058

643	LysLeuMetGlyCysAspSerPheAspGlnPheSerAlaGlu	656
2059	AAACTCATGGATGTGATTCTTCGACCAATTAGTGCAGAA	2100
657	ArgArgAsnSerIleLeuThrGluThrLeuHisArgPheSer	670
2101	AGAAGAAATTCAATCCTAACTGAGACCTTACACCGTTCTCA	2142
671	LeuGluGlyAspAlaProValSerTrpThrGluThrLysLys	684
2143	TTAGAAGGAGATGCTCCTGTCCTGGACAGAAACAAAAAAA	2184
685	GlnSerPheLysGlnThrGlyGluPheGlyGluLysArgLys	698
2185	CAATCTTTAACAGACTGGAGAGTTGGGGAAAAAGGAAG	2226
699	AsnSerIleLeuAsnProIleAsnSerIleArgLysPheSer	712
2227	AATTCTATTCTCAATCCAATCAACTCTATAACGAAAATTTC	2268
713	IleValGlnLysThrProLeuGlnMetAsnGlyIleGluGlu	726
2269	ATTGTGCAAAAGACTCCCTTACAAATGAATGGCATCGAAGAG	2310
727	AspSerAspGluProLeuGluArgArgLeuSerLeuValPro	740
2311	GATTCTGATGAGCCTTAGAGAGAAGGCTGCCTAGTACCA	2352
741	AspSerGluGlnGlyGluAlaIleLeuProArgIleSerVal	754
2353	GATTCTGAGCAGGGAGAGGCGATACTGCCTCGCATCAGCGTG	2394
755	IleSerThrGlyProThrLeuGlnAlaArgArgArgGlnSer	768
2395	ATCAGCACTGGCCCCACGCTTCAGGCACGAAGGAGGCAGTCT	2436
769	ValLeuAsnLeuMetThrHisSerValAsnGlnGlyGlnAsn	782
2437	GTCCTGAACCTGATGACACACTCAGTTAACCAAGGTCAGAAC	2478
783	IleHisArgLysThrThrAlaSerThrArgLysValSerLeu	796
2479	ATTCACCGAAAGACAACAGCATCCACACGAAAAGTGTCACTG	2520
797	AlaProGlnAlaAsnLeuThrGluLeuAspIleTyrSerArg	810
2521	GCCCCCTCAGGCAAACCTTGACTGAAGTGGATATATATTCAAGA	2562
811	ArgLeuSerGlnGluThrGlyLeuGluIleSerGluGluIle	824
2563	AGGTTATCTCAAGAAACTGGCTTGGAAATAAGTGAAGAAATT	2604
825	AsnGluGluAspLeuLysGluCysLeuPheAspAspMetGlu	838
2605	AACGAAGAAGACTAAAGGAGTGCCTTTGATGATATGGAG	2646
839	SerIleProAlaValThrThrTrpAsnThrTyrLeuArgTyr	852
2647	AGCATACCAGCAGTGAATACATGGAACACATACCTTCGATAT	2688
853	IleThrValHisLysSerLeuIlePheValLeuIleTrpCys	866
2689	ATTACTGTCCACAAAGAGCTTAATTTGTGCTAATTGGTGC	2730

867	LeuValIlePheLeuAlaGluValAlaAlaSerLeuValVal	880
2731	TTAGTAATTTCTGGCAGAGGTGGCTGCTTCTTGGTTGTG	2772
881	LeuTrpLeuLeuGlyAsnThrProLeuGlnAspLysGlyAsn	894
2773	CTGTGGCTCCTTGAAACACTCCTCTCAAGACAAAGGGAAAT	2814
895	SerThrHisSerArgAsnAsnSerTyrAlaValIleIleThr	908
2815	AGTACTCATAGTAGAAATAACAGCTATGCAGTGATTATCACCA	2856
909	SerThrSerSerTyrTyrValPheTyrIleTyrValGlyVal	922
2857	AGCACCAAGTTCGTATTATGTGTTTACATTACGTGGGAGTA	2898
923	AlaAspThrLeuLeuAlaMetGlyPhePheArgGlyLeuPro	936
2899	GCCGACACACTTGCTTGCTATGGGATTCTTCAGAGGTCTACCA	2940
937	LeuValHisThrLeuIleThrValSerLysIleLeuHisHis	950
2941	CTGGTGCATACTCTAACAGTGTGAAAATTTACACCCAC	2982
951	LysMetLeuHisSerValLeuGlnAlaProMetSerThrLeu	964
2983	AAAATGTTACATTCTGTTCTCAAGCACCTATGTCAACCCCTC	3024
965	AsnThrLeuLysAlaGlyGlyIleLeuAsnArgPheSerLys	978
3025	AACACGTTGAAAGCAGGTGGGATTCTTAATAGATTCTCCAAA	3066
979	AspIleAlaIleLeuAspAspLeuLeuProLeuThrIlePhe	992
3067	GATATAGCAATTGGATGACCTCTGCCTTACCATATT	3108
993	AspPheIleGlnLeuLeuIleValIleGlyAlaIleAla	1006
3109	GACTTCATCCAGTTGTTATTAAATTGTGATTGGAGCTATAGCA	3150
1007	ValValAlaValLeuGlnProTyrIlePheValAlaThrVal	1020
3151	GTTGTCGCAGTTTACAACCCCTACATCTTGTTGCAACAGTG	3192
1021	ProValIleValAlaPheIleMetLeuArgAlaTyrPheLeu	1034
3193	CCAGTGATAGTGGCTTTATTATGTTGAGAGCATATTCCTC	3234
1035	GlnThrSerGlnGlnLeuLysGlnLeuGluSerGluGlyArg	1048
3235	CAAACCTCACAGCAACTCAAACAACTGGAATCTGAAGGCAGG	3276
1049	SerProIlePheThrHisLeuValThrSerLeuLysGlyLeu	1062
3277	AGTCCAATTTCACTCATCTGTTACAAGCTTAAAGGACTA	3318
1063	TrpThrLeuArgAlaPheGlyArgGlnProTyrPheGluThr	1076
3319	TGGACACTTCGTGCCTCGGACGGCAGCCTACTTGAAACT	3360
1077	LeuPheHisLysAlaLeuAsnLeuHisThrAlaAsnTrpPhe	1090
3361	CTGTTCCACAAAGCTCTGAATTACATGCCAACCTGGTTC	3402

1091	LeuTyrLeuSerThrLeuArgTrpPheGlnMetArgIleGlu	1104
3403	TTGTACCTGTCAACACTGCGCTGGTCCAAATGAGAATAGAA	3444
1105	MetIlePheValIlePhePheIleAlaValThrPheIleSer	1118
3445	ATGATTTTGTCATCTTCTTCATTGCTTACCTTCATTCC	3486
1119	IleLeuThrThrGlyGluGlyGluGlyArgValGlyIleIle	1132
3487	ATTTAACAAACAGGAGAAGGAGAAGAGTGGTATTATC	3528
1133	LeuThrLeuAlaMetAsnIleMetSerThrLeuGlnTrpAla	1146
3529	CTGACTTTAGCCATGAATATCATGAGTACATTGCAGTGGGCT	3570
1147	ValAsnSerSerIleAspValAspSerLeuMetArgSerVal	1160
3571	GTAAACTCCAGCATAGATGTGGATAGCTTGATGCGATCTGT	3612
1161	SerArgValPheLysPheIleAspMetProThrGluGlyLys	1174
3613	AGCCGAGTCTTAAGTTCATTGACATGCCAACAGAACAGTAAA	3654
1175	ProThrLysSerThrLysProTyrLysAsnGlyGlnLeuSer	1188
3655	CCTACCAAGTCAACCAAACCATAACAAGAATGGCCAACCTCTCG	3696
1189	LysValMetIleIleGluAsnSerHisValLysLysAspAsp	1202
3697	AAAGTTATGATTATTGAGAATTACACGTGAAGAAAGATGAC	3738
1203	IleTrpProSerGlyGlyGlnMetThrValLysAspLeuThr	1216
3739	ATCTGGCCCTCAGGGGCCAAATGACTGTCAAAGATCTCAC	3780
1217	AlaLysTyrThrGluGlyGlyAsnAlaIleLeuGluAsnIle	1230
3781	GCAAAATACACAGAACGGTGGAAATGCCATTAGAGAACATT	3822
1231	SerPheSerIleSerProGlyGlnArgValGlyLeuLeuGly	1244
3823	TCCTTCTCAATAAGTCCTGCCAGAGGGTGGCCTCTGGGA	3864
1245	ArgThrGlySerGlyLysSerThrLeuLeuSerAlaPheLeu	1258
3865	AGAACTGGATCAGGGAAAGAGTACTTGTATCAGTTTTTG	3906
1259	ArgLeuLeuAsnThrGluGlyGluIleGlnIleAspGlyVal	1272
3907	AGACTACTGAACACTGAAGGAGAAATCCAGATCGATGGGTG	3948
1273	SerTrpAspSerIleThrLeuGlnGlnTrpArgLysAlaPhe	1286
3949	TCTTGGGATTCAATAACTTGCAACAGTGGAGGAAAGCCTT	3990
1287	GlyValIleProGlnLysValPheIlePheSerGlyThrPhe	1300
3991	GGAGTGATACCAACAGAAAGTATTATTTCTGGAACATT	4032
1301	ArgLysAsnLeuAspProTyrGluGlnTrpSerAspGlnGlu	1314
4033	AGAAAAAACTTGGATCCCTATGAACAGTGGAGTCAAGAA	4074

1315	IleTrpLysValAlaAspGluValGlyLeuArgSerValIle	1328
4075	ATATGGAAAGTTGCCAGATGAGGTTGGGCTCAGATCTGTGATA	4116
1329	GluGlnPheProGlyLysLeuAspPheValLeuValAspGly	1342
4117	GAACAGTTCTGGAAAGCTTGACTTGTCTGTGGATGGG	4158
1343	GlyCysValLeuSerHisGlyHisLysGlnLeuMetCysLeu	1356
4159	GGCTGTGTCCTAACCCATGGCCACAAGCAGTTGATGTGCTTG	4200
1357	AlaArgSerValLeuSerLysAlaLysIleLeuLeuLeuAsp	1370
4201	GCTAGATCTGTTCTCAGTAAGGCAGATCTTGCTGCTTGAT	4242
1371	GluProSerAlaHisLeuAspProValThrTyrGlnIleIle	1384
4243	GAACCCAGTGCTCATTTGGATCCAGTAACATACCAAATAATT	4284
1385	ArgArgThrLeuLysGlnAlaPheAlaAspCysThrValIle	1398
4285	AGAAGAACTCTAAAACAAGCATTGCTGATTGCACAGTAATT	4326
1399	LeuCysGluHisArgIleGluAlaMetLeuGluCysGlnGln	1412
4327	CTCTGTGAACACAGGATAGAACATGCTGGAATGCCAACAA	4368
1413	PheLeuValIleGluGluAsnLysValArgGlnTyrAspSer	1426
4369	TTTTGGTCATAGAACAGAACAAAGTGGCGAGTACGATTCC	4410
1427	IleGlnLysLeuLeuAsnGluArgSerLeuPheArgGlnAla	1440
4411	ATCCAGAAACTGCTGAACGAGAGGCCCTTCCGGCAAGCC	4452
1441	IleSerProSerAspArgValLysLeuPheProHisArgAsn	1454
4453	ATCAGCCCCCTCCGACAGGGTGAAGCTTTCCCCACCGAAC	4494
1455	SerSerLysCysLysSerLysProGlnIleAlaAlaLeuLys	1468
4495	TCAAGCAAGTGCAGTCTAACGCCCCAGATTGCTGCTGAAA	4536
1469	GluGluThrGluGluGluValGlnAspThrArgLeuEnd	1482
4537	GAGGAGACAGAAGAAGAGGGCCAAGATAACAAGGCTTAGAGA	4578
4579	GCAGCATAAAATGGTACATGGGACATTGCTCATGGAATTGG	4620
4621	AGCTCGTGGGACAGTCACCTCATGGAATTGGAGCTCGTGGAA	4662
4663	CAGTTACCTCTGCCCTCAGAAAACAAGGATGAATTAGTTT	4704
4705	TTTTAAAAAAAGAACATTGGTAAGGGGAATTGAGGACACTG	4746
4747	ATATGGGTCTTGATAATGGCTCCTGGCAATAGTCAAATTG	4788
4789	TGTGAAAGGTACTCAAATCCTGAAGATTACCACTTGCTG	4830
4831	TTTGCAGGCCAGATTTCCTGAAACCCCTGCCATGTGCTAG	4872
4873	TAATTGGAAAGGCAGCTCTAAA	4894